

Amendments to the Specification:

Please replace paragraph [0027] with the following amended paragraph:

"[0027] FIG. 6 is a stereo view of crystal structure of memapsin 2 protease domain with bound OM99-2. The polypeptide backbone of memapsin 2 is shown as a ribbon diagram. The N-lobe and C-lobe are ~~blue and yellow~~ **labeled "Blue" and "Yellow,"** respectively, except the insertion loops (designated A to G, see FIG. 6) in the C-lobe are ~~magenta~~ **labeled "Magenta"** and the C-terminal extension is ~~green~~ **labeled "Green."** The inhibitor bound between the lobes is ~~shown in red~~ **labeled "Red."**

Please replace paragraph [0028] with the following amended paragraph:

[0028] FIG. 7 is a stereo view of comparison of the three-dimensional structures of memapsin 2 and pepsin. The molecular surface of the former is significantly larger by the insertion of surface loops and helix and the C-terminal extension. Chain tracing of human memapsin 2 is ~~dark blue~~ **labeled "Dark Blue"** and is ~~grey~~ **labeled "Grey"** for human pepsin. The ~~light blue~~ balls **labeled as "Light Blue"** represent identical residues which are topologically equivalent. The disulfide bonds are ~~shown in red~~ **labeled "Red"** for memapsin 2 and ~~orange~~ **"Orange"** for pepsin. The C-terminal extension is ~~in green~~ **labeled "Green."**

Please replace paragraph [0030] with the following amended paragraph:

"[0030] FIG. 9 is a stereo presentation of interactions between inhibitor OM99-2 (~~orange~~ **labeled "Orange"**) and memapsin 2 (~~light blue~~ **labeled "Light Blue"**). Nitrogen and oxygen atoms are ~~marked blue~~ **labeled**

"Blue" and ~~red~~ "Red", respectively. Hydrogen bonds are indicated in ~~yellow~~ as dotted lines. Memapsin 2 residues which comprise the binding subsites are included. Residues P₄, P₃, P₂, P₁ and P₁' (defined in FIG. 8) of OM99-2 are in an extended conformation. Inhibitor chain turns at residue P₂' which makes a distinct kink at this position. The backbone of P₃' and P₄' directs the inhibitor to exit the active site."

Please replace paragraph [0183] with the following amended paragraph:

"[0183] About 440 solvent molecules were then gradually added to the structure as identified in the |Fo|-|Fc| map contoured at the 3 sigma level. Non-crystallographic symmetry restriction and averaging were used in early stages of refinement and model building. Bulk solvent and anisotropic over-all B factor corrections were applied through the refinement. The final structure was validated by the program PROCHECK, Laskowski, R. A. et al., J. Appl. Crystallog. 26, 283 (1993) which showed that 95% of the residues are located in the most favored region of the Ramachandran plot. All the main chain and side chain parameters are within or better than the standard criteria. The final R_{working} and R_{free} are 18% and 22% respectively. Refinement statistics of the crystallized memapsin 2 protein, residues 1-488 of SEQ ID NO: 2, are listed in Table 2."